

# Viewing Human ENCODE DNase Data

(Updated October 2013)

ENCODE has a wide variety of DNase data available for a wide assortment of cell types. The Experiment Matrix provides access to, and a quick visual summary of, what is available.

## 1) Navigate to the Human Experiment Matrix from the ENCODE portal:

Go to <http://encodeproject.org/> or the UCSC browser. Directly select the Human Experiment Matrix link (bottom arrow).

Alternatively visit the Resources & FAQ page link (top arrow) first. Notice other useful links (such as to Tutorials, Cell Types, Antibodies, Publications, and Track and File Search). Click the link to the Human Experiment Matrix.

Assays	DNA Methylation	Methyl Array	Methyl RRBS	Open Chromatin	DNase-DGF	DNase-seq	FAIRE-seq	RNA Binding Proteins	RIP Gene ST	RIP Tiling Array	RIP Validation	RIP-seq	RNA Profiling	CAGE	Exon Array	RNA-chip	RNA-PET	RNA-seq	Small RNA-seq	TFBS & Histones	ChIP-seq	Other	5C	Hi-C
Cell Types																								
Tier 1																								
GM12878	1	1		2	1	7	4		4	6	2	6	2	12	5					133			2	
H1-hESC	1	1		2		3				4	1		1	10	3					91			1	
K562	1	1		3	16	3		4	4	9	7	9	6	17	7					224			2	
Tier 2																								
A549	1	1		1	2	1				3	2		3	10	9					87				
CD20+														2	1					4				

## 2) From the Experiment Matrix click the link to the DNase-seq experiments in the Cell Type of interest, such as GM12878 (ensure tracks are selected, or select files if you want to skip viewing the data).

Cell Type	DNA Methylation	Methyl Array	Methyl RRBS	Open Chromatin	DNase-DGF	DNase-seq	FAIRE-seq	RNA Binding Proteins	RIP Gene ST	RIP Tiling Array	RIP Validation	RIP-seq	RNA Profiling	CAGE	Exon Array	RNA-chip	RNA-PET	RNA-seq	Small RNA-seq	TFBS & Histones	ChIP-seq	Other	5C	Hi-C
Tier 1																								
GM12878	1	1		2	1	7	4		4	6	2	6	2	12	5					133			2	
H1-hESC	1	1		2		3				4	1		1	10	3					91			1	
K562	1	1		3	16	3		4	4	9	7	9	6	17	7					224			2	
Tier 2																								
A549	1	1		1	2	1				3	2		3	10	9					87				
CD20+														2	1					4				

3) From the resulting Track Search page, change the visibility of the desired tracks from hide to pack (left arrow).

Search for Tracks in the Human Feb. 2009 (GRCh37/hg19) Assembly

Search **Advanced**

Track Name: contains

and Description: contains

and Group: is

and Data Format: is

and Experiment (Assay) type: is among  Experiment (Assay) type

and Cell, tissue or DNA sample: is among  Cell, tissue or DNA sample

and View - Peaks or Signals: is among

search clear cancel

View in Browser (1 of 10 selected)

Visibility	Track Name	Sort: <input type="radio"/> by Relevance <input type="radio"/> Alphabetically <input type="radio"/> by Hierarchy
<input checked="" type="checkbox"/> pack	GM12878 DNase	GM12878 DNase1 HS Uniform Peaks from ENCODE/Analysis
<input type="checkbox"/> hide	GM12878 Pk	GM12878 DNase1 HS Peaks from ENCODE/Duke
<input type="checkbox"/> hide	GM12878 DS	GM12878 DNase1 HS Density Signal from ENCODE/Duke

Alternatively, modify or add new Track Search parameters (right arrow).

4) Click the "View in Browser" button to see track displayed. Then click the left bar to click through to the related DNase Track Setting page.

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

chr10:69,641,042-69,648,262 7,221 bp

Scale chr10: 69,642,000 69,643,000 69,644,000 69,645,000 69,646,000 69,647,000 69,648,000

UCSC Genes (RefSeq, GenBank, CCDS, RefSeq, Ensembl, Comparative Genomics)

RefSeq Genes

Sequences: SHF

Human RefSeqs

Spliced ESTs: 188

Layered H3K27ac

DNase Clusters

Transcription Factor: ChIP-seq from ENCODE

Repeatmasker

move start move end

track search default tracks default order hide all add custom tracks track hubs configure reverse resize refresh

5) From the Track Setting page, you can see other track options (such as setting minimum signal value) as well as read the Track Description at the bottom of the page.

Uniform DNase1 HS Track Settings [ENCODE](#) [Downloads](#) [Subtracks](#) [Description](#) [Contact](#)

**DNase1 Hypersensitivity Uniform Peaks from ENCODE/Analysis** ([ENC DNase/FAIRE](#))

Display mode:    [Reset to defaults](#)

Minimum Signal value:  (0 to 20000)

Select all subtracks

List subtracks:  only select visible  all (1 of 125 selected)

	Tier: <sup>1</sup>	Cell Line: <sup>2</sup>	Track Name: <sup>3</sup>	
<input checked="" type="checkbox"/>	full	1 GM12878	GM12878 DNase1 HS Uniform Peaks from ENCODE/Analysis	<a href="#">schema</a>
<input type="checkbox"/>	full	1 H1-hESC	H1-hESC DNase1 HS Uniform Peaks from ENCODE/Analysis	<a href="#">schema</a>
<input type="checkbox"/>	full	1 K562	K562 DNase1 HS Uniform Peaks from ENCODE/Analysis	<a href="#">schema</a>